AGCATCCTGA	GTAATGAGTG	GCCTGGGCCG	GAGCAGGCGA	GGTGGCCGGA	GCCGTGTGGA	60
CCAGGAGGAG	CGCTTTCCAC	AGGGCCTGTG	GACGGGGGTG	GCTATGAGAT	CCTGCCCCGA	120
AGAGCAGTAC	TGGGATCCTC	TGCTGGGTAC	CTGCATGTCC	TGCAAAACCA	TTTGCAACCA	180
TCAGAGCCAG	CGCACCTGTG	CAGCCTTCTG	CAGGTCACTC	AGCTGCCGCA	AGGAGCAACG	240
CAAGTTCTAT	GACCATCTCC	TGAGGGACTG	CATCAGCTGT	GCCTCCATCT	GTGGACAGCA	300
CCCTAAGCAA	TGTGCATACT	TCTGTGAGAA	CAAGCTCAGG	AGCCCAGTGA	ACCTTCCACC	360
AGAGCTCAGG	AGACAGCGGA	GTGGAGAAGT	TGAAAACAAT	TCAGACAACT	CGGGAAGGTA	420
CCAAGGATTG	GAGCACAGAG	GCTCAGAAGC	AAGTCCAGCT	CTCCCGGGGC	TGAAGCTGAG	480
TGCAGATCAG	GTGGCCCTGG	TCTACAGCAC	GCTGGGGCTC	TGCCTGTGTG	CCGTCCTCTG	540
CTGCTTCCTG	GTGGCGGTGG	CCTGCTTCCT	CAAGAAGAGG	GGGGATCCCT	GCTCCTGCCA	600
GCCCCGCTCA	AGGCCCCGTC	AAAGTCCGGC	CAAGTCTTCC	CAGGATCACG	CGATGGAAGC	660
CGGCAGCCCT	GTGAGCACAT	CCCCCGAGCC	AGTGGAGACC	TGCAGCTTCT	GCTTCCCTGA	720
GTGCAGGGCG	CCCACGCAGG	AGAGCGCAGT	CACGCCTGGG	ACCCCCGACC	CCACTTGTGC	780
TGGAAGGTGG	GGGTGCCACA	CCAGGACCAC	AGTCCTGCAG	CCTTGCCCAC	ACATCCCAGA	840
CAGTGGCCTT	GGCATTGTGT	GTGTGCCTGC	CCAGGAGGGG	GGCCCAGGTG	CATAAATGGG	900
GGTCAGGGAG	GGAAAGGAGG	AGGGAGAGAG	ATGGAGAGGA	GGGGAGAGAG	AAAGAGAGGT	960
GGGGAGAGGG	GAGAGAGATA	TGAGGAGAGA	GAGACAGAGG	AGGCAGAAAG	GGAGAGAAAC	1020
AGAGGAGACA	GAGAGGGAGA	GAGAGACAGA	GGGAGAGAGA	GACAGAGGGG	AAGAGAGGCA	1080
GAGAGGGAAA	GAGGCAGAGA	AGGAAAGAGA	CAGGCAGAGA	AGGAGAGAGG	CAGAGAGGGA	1140
GAGAGGCAGA	GAGGGAGAGA	GGCAGAGAGA	CAGAGAGGGA	GAGAGGGACA	GAGAGAGATA	1200
GAGCAGGAGG	TCGGGGCACT	CTGAGTCCCA	GTTCCCAGTG	CAGCTGTAGG	TCGTCATCAC	1260
CTAACCACAC	GTGCAATAAA	GTCCTCGTGC	CTGCTGCTCA	CAGCCCCCGA	GAGCCCCTCC	1320
TCCTGGAGAA	TAAAACCTTT	GGCAGCTGCC	CTTCCTCAAA	AAAAAAAAAA	AAAAAAA	1377

FIGURE 1A

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
1 5 10 15

Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
20 25 30

Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
35 40 45

Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
50 55 60

Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
65 70 75 80

His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
85 90 95

Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
100 105 110

Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
115 120 125

Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
130 135 140

Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
145 150 155 160

Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
165 170 175

Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
180 185 190

Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
195 200 205

Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
210 215 220

Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
225 230 235 240

Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
245 250 255

Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
260 265 270

His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
275 280 285

Gly Gly Pro Gly Ala
290

FIGURE 1B

(start and stop codons are in bold type)

AGCAAGTTCA GCCTGGTTAA GTCCAAGCTG AATTCCGGTC AAAGTTCAAG
TAGTGAT**ATG** GATGACTCCA CAGAAAGGGA GCAGTCACGC CTTACTTCTT
GCCTTAAGAA AAGAGAAGAA ATGAAACTGA AGGAGTGTGT TTCCATCCTC
CCACGGAAGG AAAGCCCCTC TGTCCGATCC TCCAAAGACG GAAAGCTGCT
GGCTGCAACC TTGCTGCTGG CACTGCTGTC TTGCTGCCTC ACGGTGGTGT
CTTTCTACCA GGTGGCCGCC CTGCAAGGGG ACCTGGCCAG CCTCCGGGCA
GAGCTGCAGG GCCACCACGC GGAGAAGCTG CCAGCAGGAG CAGGAGCCCC
CAAGGCCGGC CTGGAGGAAG CTCCAGCTGT CACCGCGGGA CTGAAAATCT
TTGAACCACC AGCTCCAGGA GAAGGCAACT CCAGTCAGAA CAGCAGAAAT
AAGCGTGCCG TTCAGGGTCC AGAAGAAACA GTCACTCAAG ACTGCTTGCA
ACTGATTGCA GACAGTGAAA CACCAACTAT ACAAAAAGGA TCTTACACAT
TTGTTCCATG GCTTCTCAGC TTTAAAAGGG GAAGTGCCCT AGAAGAAAAA
GAGAATAAAA TATTGGTCAA AGAAACTGGT TACTTTTTTA TATATGGTCA
GGTTTTATAT ACTGATAAGA CCTACGCCAT GGGACATCTA ATTCAGAGGA
AGAAGGTCCA TGTCTTTGGG GATGAATTGA GTCTGGTGAC TTTGTTTCGA
TGTATTCAAA ATATGCCTGA AACACTACCC AATAATTCCT GCTATTCAGC
TGGCATTGCA AAACTGGAAG AAGGAGATGA ACTCCAACTT GCAATACCAA
GAGAAAATGC ACAAATATCA CTGGATGGAG ATGTCACATT TTTTGGTGCA
TTGAAACTGC TGTGACCTAC TTACACCATG TCTGTAGCTA TTTTCCTCCC
TTTCTCTGTA CCTCTAAGAA GAAAGAATCT AACTGAAAAT ACCAAAAAAA
AAAAAAAAAA AAAAAGATCT TTAATTAAGC GGCCGCAAGC TTATTCCCTT
TAGTGAG

FIGURE 2A

Translation in relevant reading frame (3' 5'):

MDDSTEREQS RLTSCLKKRE EMKLKECVSI LPRKESPSVR SSKDGKLLAA
TLLLALLSCC LTVVSFYQVA ALQGDLASLR AELQGHHAEK LPAGAGAPKA
GLEEAPAVTA GLKIFEPPAP GEGNSSQNSR NKRAVQGPEE TVTQDCLQLI
ADSETPTIQK GSYTFVPWLL SFKRGSALEE KENKILVKET GYFFIYGQVL
YTDKTYAMGH LIQRKKVHVF GDELSLVTLF RCIQNMPETL PNNSCYSAGI
AKLEEGDELQ LAIPRENAQI SLDGDVTFFG ALKLL

FIGURE 2B

Translation in relevant reading frame (3' 5'):

MARRLWILSL LAVTLTVALA APSQKSKRRT SSDRMKQIED KIEEILSKIY
HIENEIARIK KLIGERTRSG NSSQNSRNKR AVQGPEETVT QDCLQLIADS
ETPTIQKGSY TFVPWLLSFK RGSALEEKEN KILVKETGYF FIYGQVLYTD
KTYAMGHLIQ RKKVHVFGDE LSLVTLFRCI QNMPETLPNN SCYSAGIAKL
EEGDELQLAI PRENAQISLD GDVTFFGALK LL
(SEQ ID NO:3)

FIGURE 3

FEB2499B 25-FEB-99 14:56 Page 1

Plate Binding assay-NLLZ + HuTACIFc (Goat anti-human Fc) 1/6/99
25-FEB-99

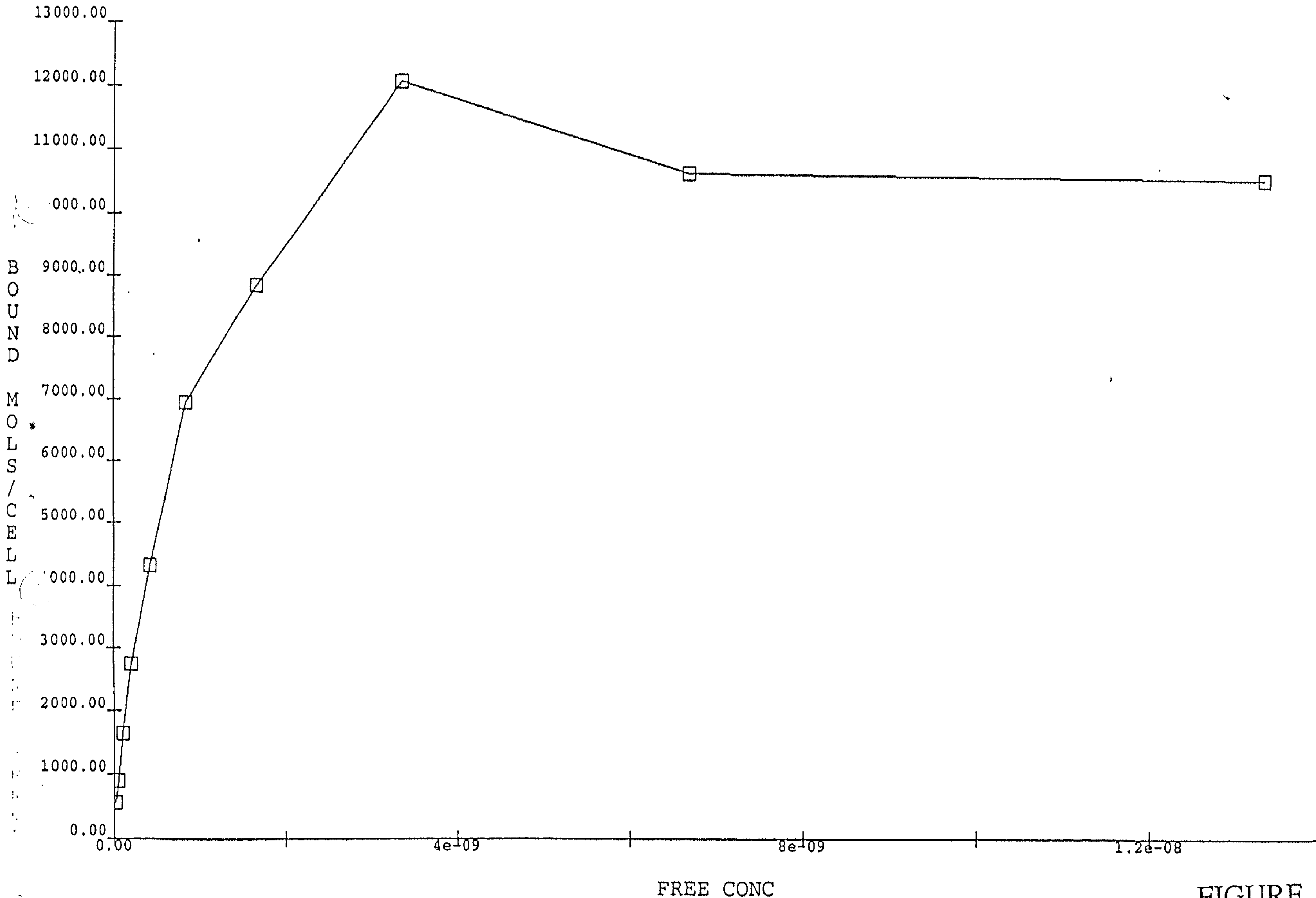


FIGURE 4A

FEB2499C

25-FEB-99 14:56 Page 1

1:2 dil.

Plate Binding assay-NLLZ + HuTACIFc (Goat anti-human Fc) 1/6/99
25-FEB-99

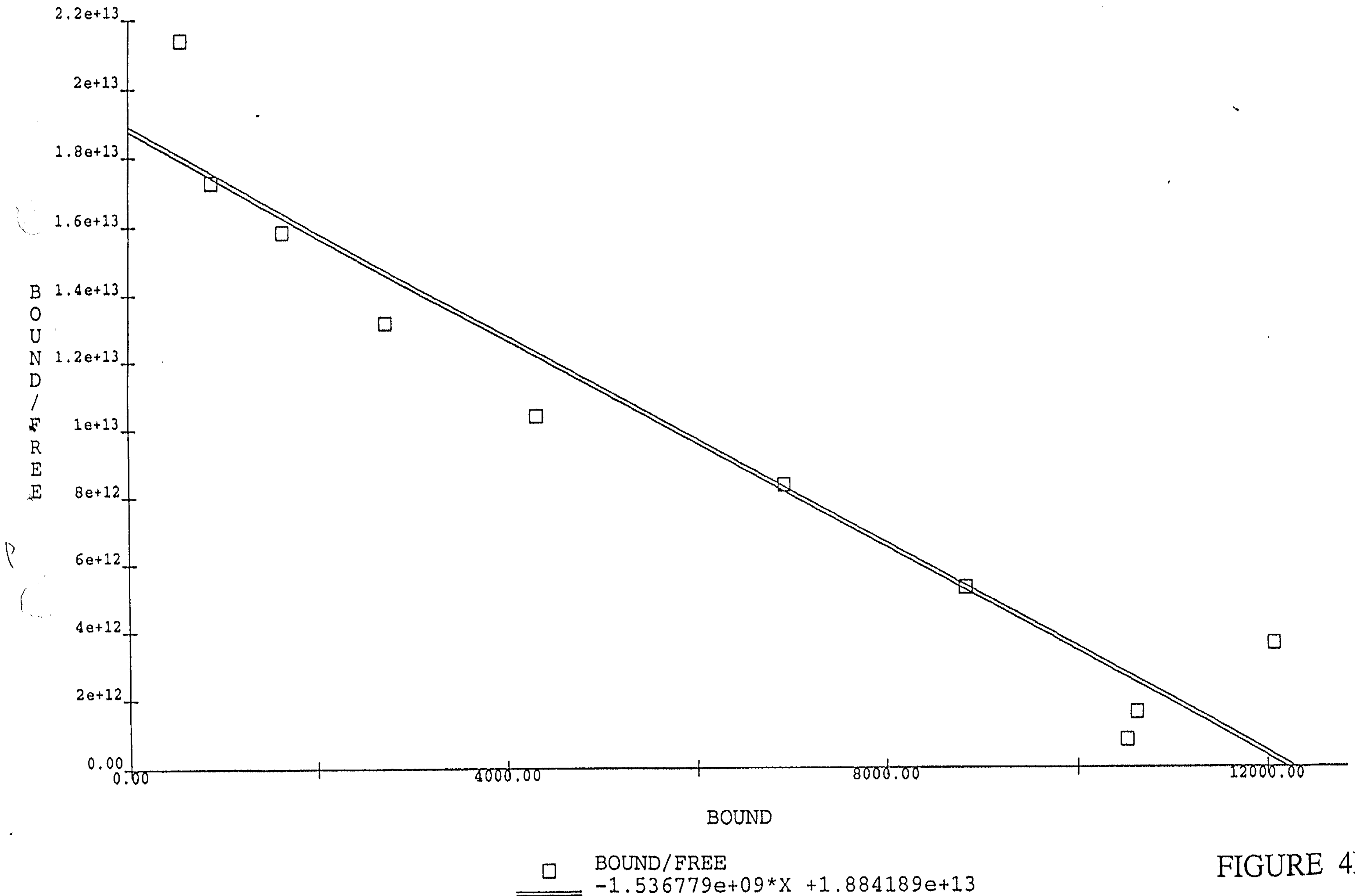


FIGURE 4B

Ka = 1.536779e+09

CFEB2499C

1:5 dil.

Plate Binding assay-NLLZ + HuTACIFc (Goat anti-hu Fc) 1/6/99 duplicate
25-FEB-99

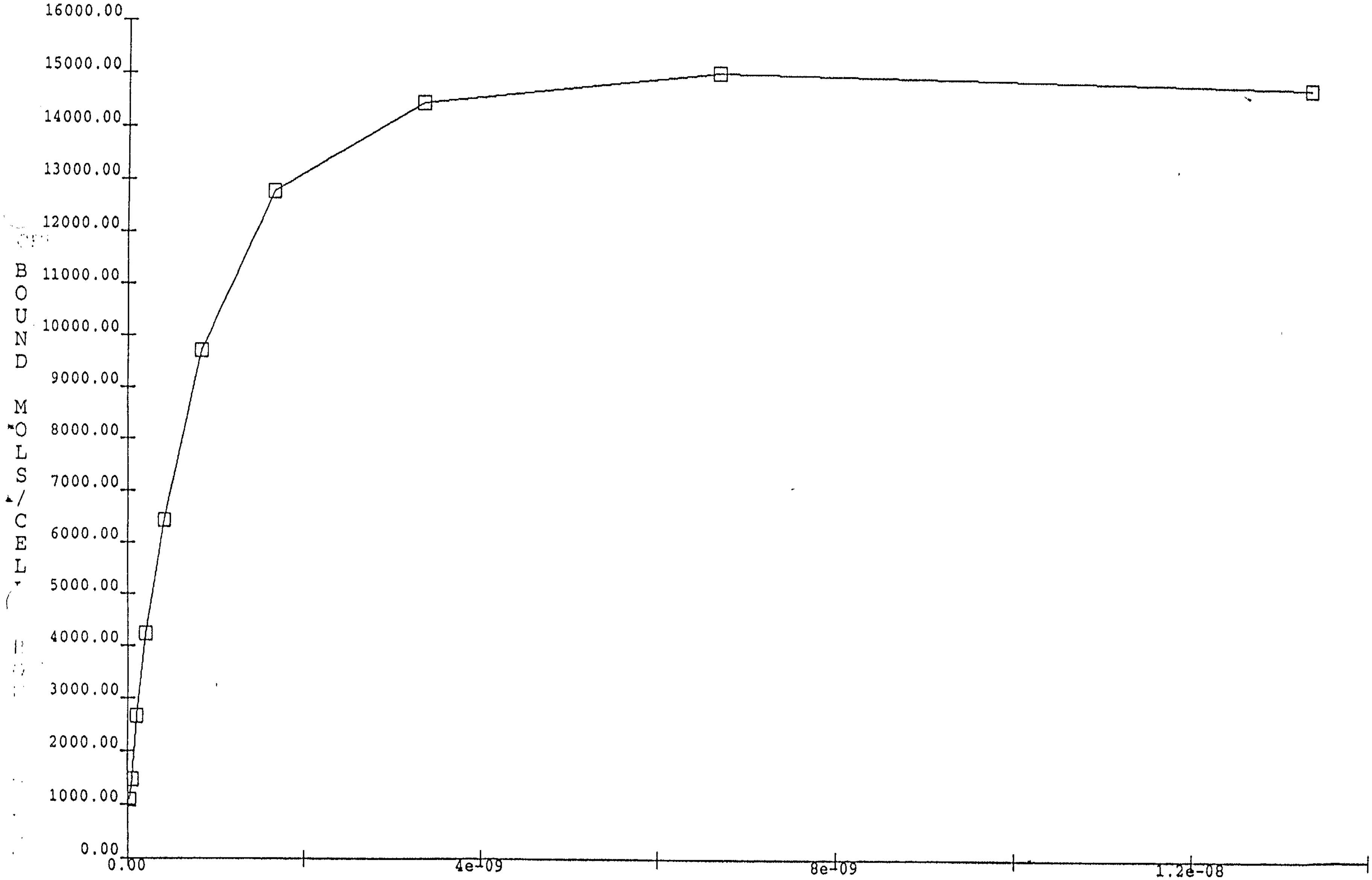


FIGURE 5A

CFEB2499D

25-FEB-99 14:57 Page 1

1:5 dil.

Plate Binding assay-NLLZ + HuTACIFc (Goat anti-hu Fc) 1/6/99 duplicate
25-FEB-99

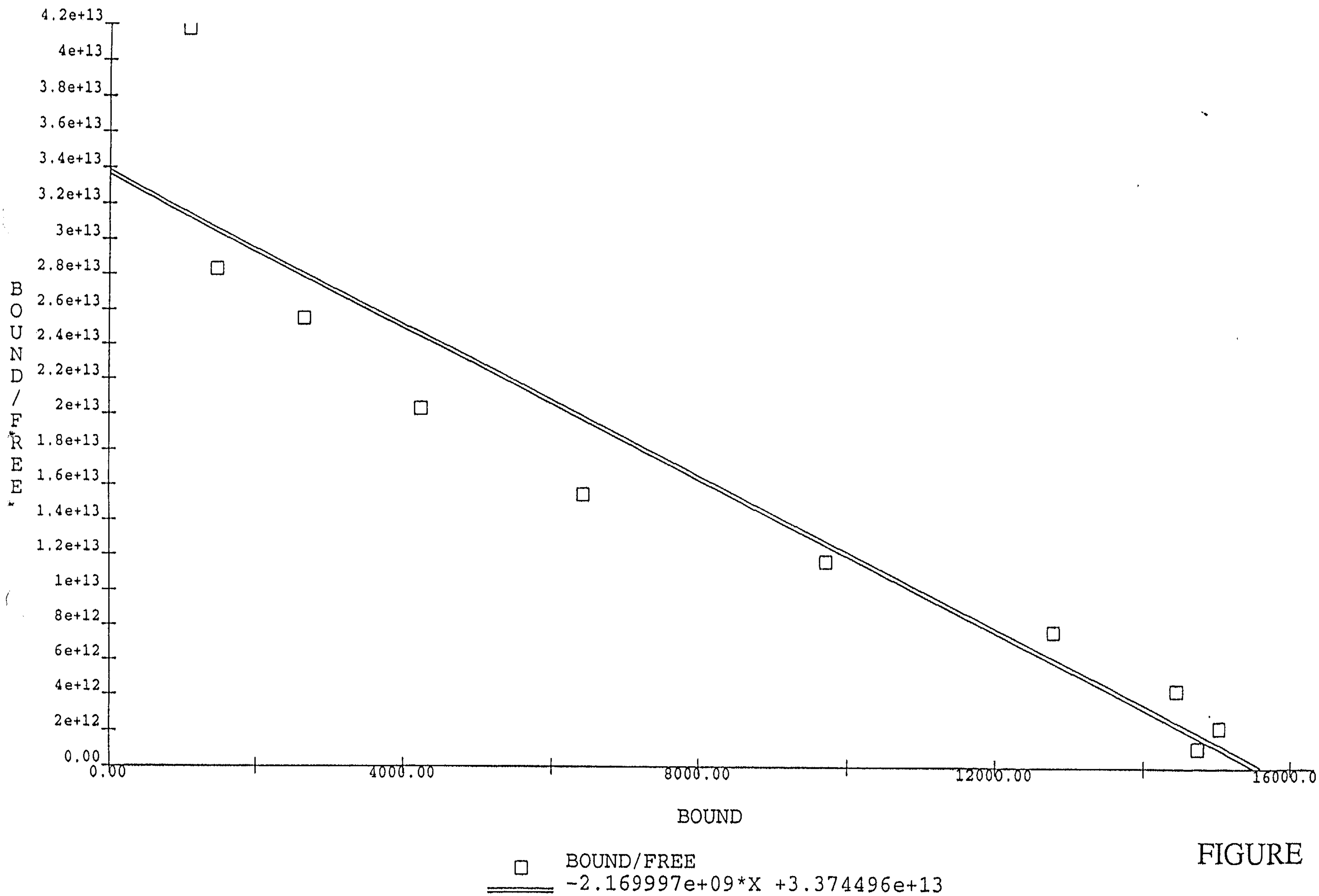


FIGURE 5B

Ka = 2.169997e+09

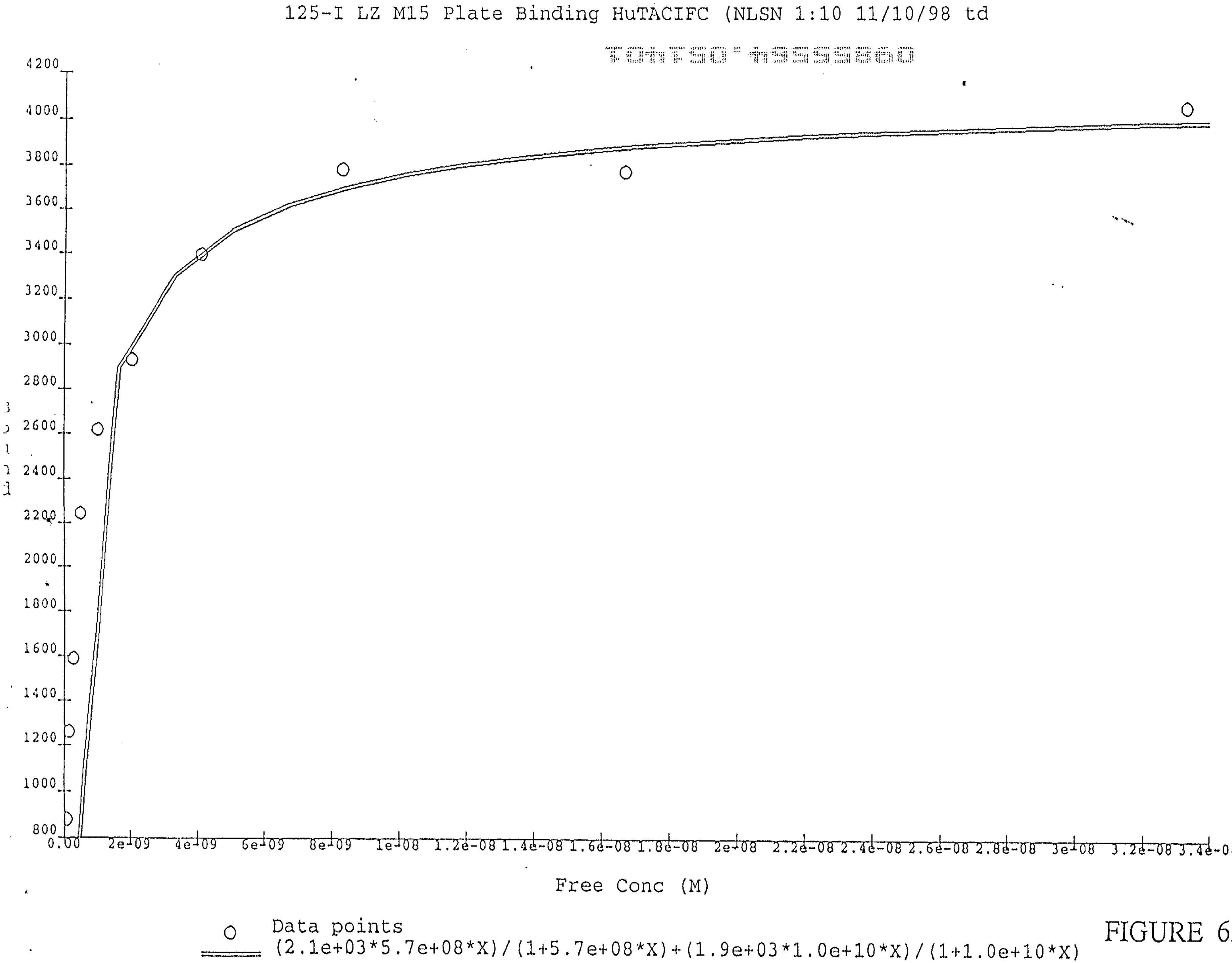
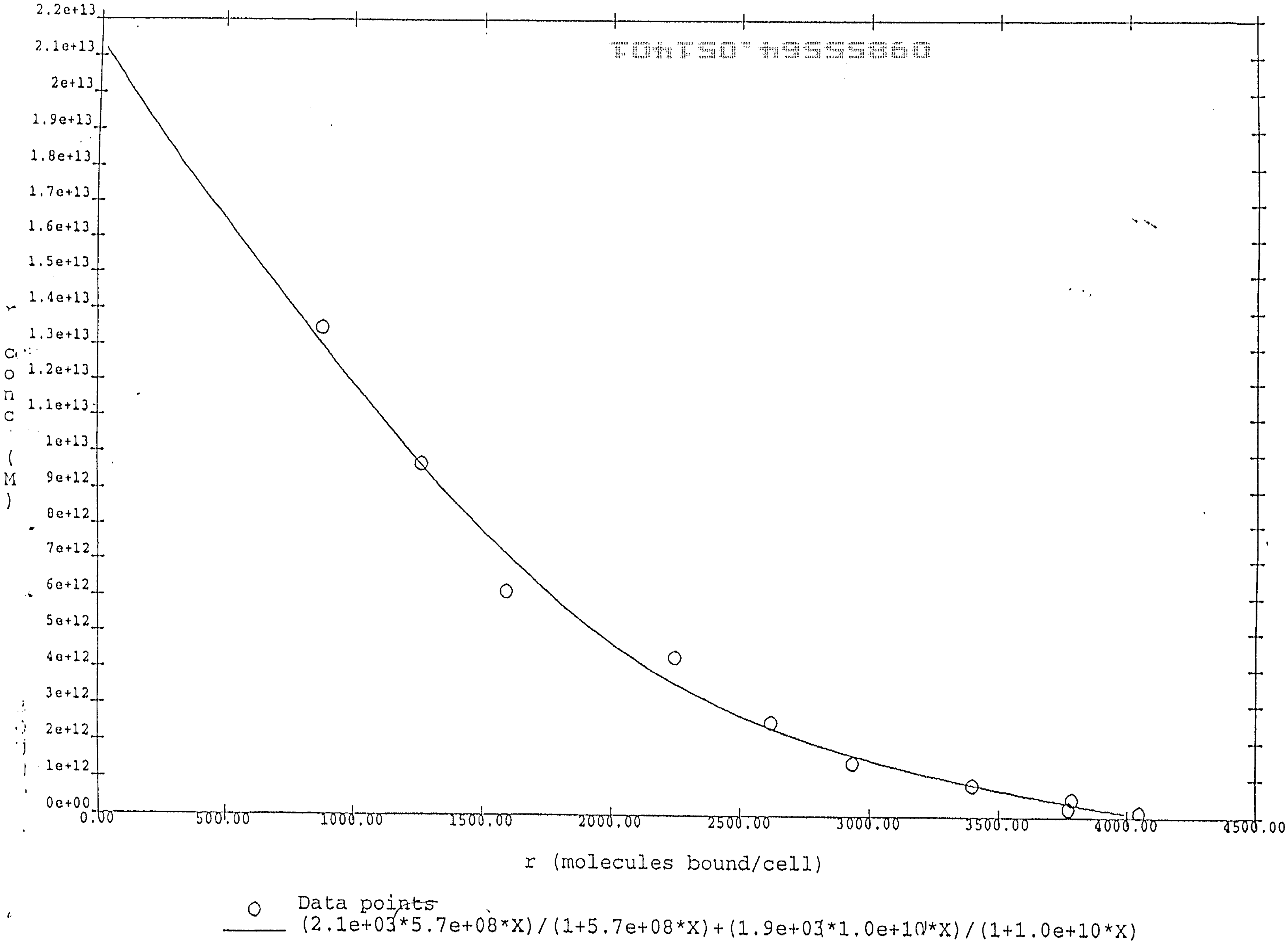

125-I LZ M15 Plate Binding HuTACIFC (NLSN 1:10 11/10/98 td
4200
4000
3800
3600
3400
3200
3000
2800
2600
2400
2200
2000
1800
1600
1400
1200
1000
800
0.00
2e-09
4e-09
6e-09
8e-09
1e-08
1.2e-08
1.4e-08
1.6e-08
1.8e-08
2e-08
2.2e-08
2.4e-08
2.6e-08
2.8e-08
3e-08
3.2e-08
3.4e-08
Free Conc (M)
Data points
(2.1e+03*5.7e+08*X)/(1+5.7e+08*X)+(1.9e+03*1.0e+10*X)/(1+1.0e+10*X)

FIGURE 6A



2.2e+13
2.1e+13
2e+13
1.9e+13
1.8e+13
1.7e+13
1.6e+13
1.5e+13
1.4e+13
1.3e+13
1.2e+13
1.1e+13
1e+13
9e+12
8e+12
7e+12
6e+12
5e+12
4e+12
3e+12
2e+12
1e+12
0e+00
r conc (M)
0.00
500.00
1000.00
1500.00
2000.00
2500.00
3000.00
3500.00
4000.00
4500.00
r (molecules bound/cell)
Data points
(2.1e+03*5.7e+08*X)/(1+5.7e+08*X)+(1.9e+03*1.0e+10*X)/(1+1.0e+10*X)

FIGURE 6B